



Year: 2017

Wastewater is a reservoir for clinically relevant carbapenemase and 16S rRNA methylase producing Enterobacteriaceae

Zurfluh, Katrin ; Bagutti, Claudia ; Brodmann, Peter ; Alt, M ; Schulze, J ; Fanning, S ; Stephan, Roger

Abstract: The aim of this study was to evaluate wastewater for carbapenemase-producing Enterobacteriaceae (CPE) and 16S rRNA methylase-producing Gram-negative bacteria (MPB) and to assess their occurrence following wastewater treatment. Wastewater samples were collected between June 2015 and March 2016 in the sewage network of the city of Basel (Switzerland) from sites located before and after influx of wastewater from the hospital into the sewage network. Samples were also obtained from the influent and effluent of the receiving wastewater treatment plant. Samples were screened for CPE and MPB using selective media. *Escherichia coli* and *Klebsiella pneumoniae* were typed by multilocus sequence typing (MLST). Carbapenemase and 16S rRNA methylase genes were identified by PCR and sequencing. Resistance profiles were determined by the disk diffusion test and Etest. The occurrence of CPE and MPB was increased downstream of hospital wastewater influx. Of 49 CPE isolates, 9 belonged to OXA-48-producing *E. coli* clone D:ST38, 7 were OXA-48-producing *Citrobacter freundii*, and 6 were KPC-2- or OXA-48-producing *K. pneumoniae* belonging to clonal complex 258. NDM (NDM-1, -5 and -9) and VIM (VIM-1) producers were detected sporadically. MPB included ArmA- and RmtB-producing *E. coli* and *Citrobacter* spp. Isolates corresponding to strains from wastewater were detected in the effluent of the treatment plant. Conclusively, CPE and MPB, predominantly OXA-48-producing Enterobacteriaceae, are readily detected in wastewater, survive wastewater treatment and are released into the aquatic environment. OXA-48-producers may represent an emerging threat to public health and environmental integrity.

DOI: <https://doi.org/10.1016/j.ijantimicag.2017.04.017>

Posted at the Zurich Open Repository and Archive, University of Zurich

ZORA URL: <https://doi.org/10.5167/uzh-149080>

Journal Article

Accepted Version



The following work is licensed under a Creative Commons: Attribution-NonCommercial-NoDerivatives 4.0 International (CC BY-NC-ND 4.0) License.

Originally published at:

Zurfluh, Katrin; Bagutti, Claudia; Brodmann, Peter; Alt, M; Schulze, J; Fanning, S; Stephan, Roger (2017). Wastewater is a reservoir for clinically relevant carbapenemase and 16S rRNA methylase producing Enterobacteriaceae. *International Journal of Antimicrobial Agents*, 50(3):436-440.

DOI: <https://doi.org/10.1016/j.ijantimicag.2017.04.017>

Wastewater is a reservoir for clinically relevant carbapenemase- and 16S rRNA methylase-producing Enterobacteriaceae

Katrin Zurfluh ^a, Claudia Bagutti ^b, Peter Brodmann ^b, Monica Alt ^b, Jürg Schulze ^b, Séamus Fanning ^c, Roger Stephan ^{a,*}, Magdalena Nüesch-Inderbinen ^a

^a *Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 272, CH-8057 Zurich, Switzerland*

^b *State Laboratory of Basel-Stadt, Kannenfeldstrasse 2, 4056 Basel, Switzerland*

^c *UCD–Centre for Food Safety, School of Public Health, Physiotherapy & Sports Science, University College Dublin, Belfield, Dublin 4, Ireland*

ARTICLE INFO

Article history:

Received 2 December 2016

Accepted 12 April 2017

Keywords:

Carbapenems

Aminoglycosides

Resistance

Wastewater

* Corresponding author. Tel.: +41 44 635 8651; fax: +41 44 635 8908.

E-mail address: stephanr@fsafety.uzh.ch (R. Stephan).

ABSTRACT

The aim of this study was to evaluate wastewater for carbapenemase-producing Enterobacteriaceae (CPE) and 16S rRNA methylase-producing Gram-negative bacteria (MPB) and to assess their occurrence following wastewater treatment. Wastewater samples were collected between June 2015 and March 2016 in the sewage network of the city of Basel (Switzerland) from sites located before and after influx of wastewater from the hospital into the sewage network. Samples were also obtained from the influent and effluent of the receiving wastewater treatment plant. Samples were screened for CPE and MPB using selective media. *Escherichia coli* and *Klebsiella pneumoniae* were typed by multilocus sequence typing (MLST). Carbapenemase and 16S rRNA methylase genes were identified by PCR and sequencing. Resistance profiles were determined by the disk diffusion test and Etest. The occurrence of CPE and MPB was increased downstream of hospital wastewater influx. Of 49 CPE isolates, 9 belonged to OXA-48-producing *E. coli* clone D:ST38, 7 were OXA-48-producing *Citrobacter freundii*, and 6 were KPC-2- or OXA-48-producing *K. pneumoniae* belonging to clonal complex 258. NDM (NDM-1, -5 and -9) and VIM (VIM-1) producers were detected sporadically. MPB included ArmA- and RmtB-producing *E. coli* and *Citrobacter* spp. Isolates corresponding to strains from wastewater were detected in the effluent of the treatment plant. Conclusively, CPE and MPB, predominantly OXA-48-producing Enterobacteriaceae, are readily detected in wastewater, survive wastewater treatment and are released into the aquatic environment. OXA-48-producers may represent an emerging threat to public health and environmental integrity.

1. Introduction

Dissemination of carbapenemase-producing Enterobacteriaceae (CPE) is a major concern for healthcare providers worldwide. Carbapenemases are β -lactamases, usually plasmid-encoded, that hydrolyse almost all β -lactam antibiotics. Most CPE are also resistant to multiple other classes of antimicrobials and therefore treatment options for infections are limited. Among the few remaining antimicrobials, tigecycline, fosfomycin, colistin and aminoglycoside antibiotics (mainly gentamicin) are the currently considered chemotherapeutic options for the treatment of severe infections caused by multidrug-resistant (MDR) CPE [1]. However, high-level resistance to aminoglycosides owing to the production of plasmid-encoded 16S rRNA methylase is emerging in Enterobacteriaceae and may be associated with the production of carbapenemases [2]. Clinically relevant carbapenemases include the class A KPC, the class B metallo- β -lactamases VIM, IMP and NDM, and the class D OXA-48-type enzymes [3]. In the hospital setting in Switzerland, CPE are isolated predominantly from patients exposed via previous contact with healthcare services in CPE-endemic countries such as India, Cyprus, Greece and Italy, whereby the most important carbapenemase-producing species continues to be *Klebsiella pneumoniae* [4,5]. However, the last years have seen the emergence of other carbapenemase-producing species such as *Escherichia coli*, *Enterobacter* spp. and *Citrobacter* spp. The development of resistance to carbapenems among *E. coli* is of particular concern because of its potential to disseminate carbapenemases to the community and the environment generally, a situation analogous to the global spread of extended-spectrum β -lactamases (ESBLs), especially of *E. coli* sequence type (ST) 131 harbouring *bla*_{CTX-M-15}, during the last decade [4]. One of the most pressing challenges is to determine reservoirs and transmission pathways of CPE and other

MDR bacteria in order to reduce the risk to public health. Wastewater has repeatedly been described to reflect the current status of antibiotic-resistant bacteria in the population [6,7]. Hospital wastewater (HWW) is reported to serve as an important reservoir of CPE [8], however the correlation between clinical isolates of CPE and CPE isolated from HWW remains unclear [9,10]. The aim of this study was to evaluate the presence of CPE and 16S rRNA methylase-producing bacteria (MPB) in wastewater. Samples were collected over a 9-month period from different sites within the sewage disposal network of the city of Basel, Switzerland. The sites under scrutiny corresponded to municipal wastewater (MWW), HWW, treatment plant influent (TPI) and treatment plant effluent (TPE). Isolates were examined for (i) species identity, phylogenetic group or multilocus sequence type (MLST), (ii) carbapenemase or 16S rRNA methylase genes, ESBL genes and the plasmid-mediated colistin resistance gene *mcr-1* and (iii) antimicrobial susceptibility profile.

2. Materials and methods

2.1. Study setting and sampling

This study targeted multiple sites within the sewage disposal network of the city of Basel, including sites sampled upstream and downstream of the wastewater discharge of the University Hospital of Basel, a tertiary care centre admitting more than 32 000 adult patients per year. Wastewater accrues from the city of Basel, which has a current population of 190 000, as well as 11 surrounding communities, excluding wastewater from the chemical and pharmaceutical industry, which is treated in a separate chemical wastewater treatment plant (WWTP). The WWTP processes 100 million litres of raw sewage per day using a primary sedimentation

basin, secondary biological treatment tanks and a final secondary sedimentation basin. Treated water is released directly into the River Rhine.

Sampling took place on seven occasions between June 2015 and March 2016.

Sewage water samples were taken from a total of 10 sites, representing four different types of wastewater: four sampling sites (denoted as sites I–IV), representing MWW, were located ca. 250, 330, 500 and 730 m upstream of four sewage discharge sites of the University Hospital Basel. Four sampling sites (denoted as V–VIII), representing HWW, were located immediately downstream of the four hospital discharge sites. Sampling site IX, representing wastewater TPI, was located at the inlet of the WWTP, at a distance of ca. 4000 m from sites V–VIII. Sampling site X, representing TPE, was situated at the final outlet channel of the WWTP.

For analysis of MWW and HWW, samples from sites I–IV and sites V–VIII, respectively, were pooled on each sampling occasion.

2.2. Bacterial isolation

For each water sample, 50 mL was passed through a 0.45 µm filter (Millipore, Billerica, MA). Filters were incubated for 24 h at 37 °C in 10 mL of Enterobacteriaceae enrichment broth (Becton Dickinson, Heidelberg, Germany) for enrichment. Screening for CPE was performed by streaking one loopful of enriched culture onto chromID® CARBA SMART and one loopful onto chromID® OXA-48 (bioMérieux, Marcy-l'Étoile, France). Screening for aminoglycoside-resistant Gram-negative bacteria was conducted using **Luria Bertani agar (Difco Laboratories,**

Franklin Lakes NJ, USA) containing amikacin (200 mg/L), vancomycin (10 mg/L) and amphotericin B (5 mg/L). All colonies with different morphologies were picked, subcultured and purified on chromID® CARBA SMART/chromID® OXA-48 or on selective medium with amikacin, respectively. Oxidase-negative, presumptive carbapenemase-producers were further subcultured on Müller–Hinton agar (Becton Dickinson, Allschwil, Switzerland) plates and were subsequently screened for carbapenemase activity using the RAPIDEC® CARBA NP test (bioMérieux). Isolates were subjected to identification by protein profiling using matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF/MS) (AXIMA Confidence; Shimadzu-Biotech Corp., Kyoto, Japan) using SARAMIS™ Database (Spectral Archive and Microbial Identification System; AnagnosTec, Potsdam-Golm, Germany) and PAPMID Database (Mabritec SA, Riehen, Switzerland). Strains yielding doubtful results were subjected to genetic identification based on sequencing of the *rpoB* gene fragment [11].

2.3. Phylogenetic classification of *Escherichia coli* isolates

Each *E. coli* isolate was assigned to one of the four phylogenetic groups designated A, B1, B2 or D using PCR as described previously [12], whereby group A and B1 typically contain commensal *E. coli* strains, whilst groups B2 and D consist of virulent extraintestinal strains.

2.4. Multilocus sequence typing of *Escherichia coli* and *Klebsiella pneumoniae*

For MLST of *E. coli* isolates, internal fragments of seven housekeeping genes (*adh*, *fumC*, *gyrB*, *icd*, *mdh*, *purA* and *recA*) were amplified by PCR and were sequenced

as described by Wirth et al. [13]. Sequences were imported into the *E. coli* MLST database website (<http://mlst.ucc.ie/mlst/dbs/Ecoli>) to determine sequence types (STs).

MLST of the *K. pneumoniae* isolates was performed by PCR amplification and sequencing of seven housekeeping genes (*gapA*, *infB*, *mdh*, *pgi*, *phoE*, *rpoB* and *tonB*) according to previously described methods [14]. STs were determined according to the MLST database (<http://bigsd.b.pasteur.fr/klebsiella/>).

Alleles and STs that had not been previously described were submitted to the curators of the databases and were assigned new designations.

2.5. Detection of antimicrobial resistance genes

DNA was extracted by a standard heat lysis protocol and was analysed by PCR for the presence of antimicrobial resistance genes. Synthesis of primers and custom DNA sequencing were carried out by Microsynth (Balgach, Switzerland). Purification of amplicons was performed using a PCR purification kit (Sigma-Aldrich, Buchs, Switzerland). All presumptive carbapenemase-producers were screened for the presence of *bla*_{VIM}, *bla*_{KPC}, *bla*_{NDM-1} and *bla*_{OXA-48} using previously described primers [15,16].

Isolates exhibiting an ESBL phenotype were screened for *bla*_{TEM}, *bla*_{SHV} and *bla*_{CTX-M} genes using previously published primers [17,18]. Presumptive 16S rRNA methylase-producers were analysed for the presence of *armA*, *rmtA*, *rmtB*, *rmtC* and *rmtD* as described previously [19]. All isolates were screened for the presence of the

plasmid-mediated colistin resistance gene *mcr-1* using primers published recently [20]. Nucleotide sequences were analysed with CLC Main Workbench 7.7 (CLC bio, Aarhus, Denmark). Database searches were performed using the BLASTN program of the National Center for Biotechnology Information (NCBI) (<http://www.ncbi.nlm.nih.gov/blast/>).

2.6. Antimicrobial susceptibility testing

Minimum inhibitory concentrations (MIC) of imipenem, ertapenem and meropenem for CPE and of amikacin, kanamycin and gentamicin for MPB were determined by Etest (bioMérieux) according to the manufacturer's instructions and Clinical and Laboratory Standards Institute (CLSI) evaluation criteria [21]. All isolates were tested for susceptibility to 13 antimicrobial agents by the disk diffusion method. Zone diameters were determined and evaluated according to CLSI protocols and criteria [21]. The antibiotics tested were ampicillin, amoxicillin/clavulanic acid, cefalotin, cefotaxime, nalidixic acid, ciprofloxacin, gentamicin, kanamycin, streptomycin, sulfamethoxazole, trimethoprim, chloramphenicol and tetracycline (Becton Dickinson, Heidelberg, Germany). Multidrug resistance was defined as resistance to three or more classes of antimicrobials.

3. Results

3.1. Detection and characterisation of bacteria

Presumptive carbapenemase-producers were recovered from all wastewater types within the sewage disposal network (Table 1; Supplementary Table S1). A total of 2 CPE isolates were retrieved from MWW, 23 from HWW, 10 from TPI and 14 from

TPE. In total 49 CPE isolates were retrieved, including 21 *E. coli*, 12 *K. pneumoniae*, 8 *Citrobacter freundii*, 1 *Citrobacter youngae*, 5 other *Citrobacter* spp., 1 *Enterobacter aerogenes* and 1 *Enterobacter cloacae*. Typing of the *E. coli* isolates placed 10 (47.6%) within phylogenetic group A and clonal complex (CC) 10, and 9 (42.9%) within phylogenetic group D and CC38. The remaining isolates belonged to various STs (Table 1). Typing of the *K. pneumoniae* isolates identified six (50%) belonging to CC258. Other STs, including two new types ST2256 and ST2257, are listed in Table 1. No *E. coli* B2:ST131 clones were identified in any of the wastewater samples.

Isolates expressing high resistance to aminoglycosides were recovered from HWW, TPI and TPE. These isolates were identified as *E. coli* ($n = 8$), belonging to ST10, ST635, ST648 and ST1266, and *Citrobacter* spp. ($n = 2$) (Table 1).

3.2. Characterisation of antimicrobial resistance genes

All detected resistance genes are listed in Supplementary Table S1. The majority of CPE isolates (35/49; 71.4%) from the chromID® CARBA SMART/chromID® OXA-48 plates harboured *bla*_{OXA-48}. Six (12.2%) of the isolates were *bla*_{NDM}-producers (two *bla*_{NDM-1}, three *bla*_{NDM-5} and one *bla*_{NDM-9}). Five (10.2%, all *K. pneumoniae*) isolates tested positive for *bla*_{KPC}, three (6.1%) contained *bla*_{OXA-181} and four (8.2%) harboured *bla*_{VIM} (Table 1). Four (8.2%) of the isolates produced more than one carbapenemase: one *E. coli* D:ST393 and one *C. freundii* strain possessed both *bla*_{OXA-48} and *bla*_{VIM-1}. Similarly, two *Citrobacter* spp. carried both *bla*_{OXA-48} and *bla*_{NDM-1}. Twenty-five (51.0%) of the CPE isolates also contained *bla*_{CTX-M} genes. Of these, 14 (56.0%) were *bla*_{CTX-M-15}, 6 (24.0%) were *bla*_{CTX-M-3}, 3 (12.0%) were *bla*_{CTX-}

M-24 and 2 (8.0%) were *bla*_{CTX-M-14}. Two (4.1%) of the 49 CPE contained *bla*_{SHV-12}.

The gene *bla*_{CTX-M-3} was observed only in *Citrobacter* spp., and *bla*_{SHV-12} was detected in *Citrobacter* spp. (Supplementary Table S1). The two *bla*_{NDM-1} harbouring *Citrobacter* spp. isolates were additionally tested for the presence of 16S rRNA methylase genes, and *armA* was detected (Table 1).

Of the eight methylase-producing *E. coli* strains isolated from the selective medium with amikacin, five (62.5%) harboured *rmtB* and three (37.5%) contained *armA* (Table 1). Furthermore, one isolate contained *bla*_{NDM-5}, one possessed *bla*_{CTX-M-65} and two isolates contained *bla*_{CTX-M-55} and *bla*_{CTX-M-65}, respectively (Supplementary Table S1).

None of the CPE or MPB possessed the colistin resistance gene *mcr-1*.

3.3. Antimicrobial susceptibility profiles

MICs and the results of the disk diffusion tests for each isolate are listed in Supplementary Table S1. Regarding multidrug resistance, 39 (79.6%) of the 49 CPE and all 10 (100%) MPB were MDR. Six (28.6%) carbapenemase-producing *E. coli* (four NDM, one VIM-1 and one OXA-181 producer) and seven (58.3%) *K. pneumoniae* (five KPC, one OXA-48 and one NDM-9 producer) exhibited resistance to one or more carbapenems. Of the 35 OXA-48-producers, 5 (14.3%) were classified as resistant to one or more carbapenems according to current CLSI guidelines.

3.4. Isolation frequency for sampling occasions

A large proportion of the study isolates (19 of the CPE and 2 of the MPB) were retrieved sporadically (on one sampling occasion each). CPE that were detected on two occasions included *K. pneumoniae* belonging to CC258, RmtB-producing *E. coli* A:ST10 and ArmA-producing *E. coli* B2:ST1266 (Table 1). OXA-48-producing *C. freundii* were recovered on four sampling occasions and from HWW, TPI and TPE. The most frequently encountered clone, OXA-48-producing *E. coli* D:ST38, was isolated on five occasions and was the only clone detected simultaneously in MWW, HWW, TPI and TPE.

4. Discussion

This study was carried out to determine the occurrence of CPE and MPB at different sites of the sewage disposal network of the city of Basel, Switzerland, including before and after influx of wastewater from the hospital into the sewage network and the WWTP. Whilst the presence of CPE and other antimicrobial-resistant bacteria in HWW and within treatment plants is reported in the literature [9,22,23], little is known so far about the presence of CPE in MWW. In this study, MWW contained NDM-5-producing *E. coli* A:ST617. NDM-5 was first described in a clinical *E. coli* clone ST648 isolate in the UK in 2011 [24]. To our knowledge, NDM-5 has not been described in ST617 before and its identification not only in MWW but also in TPI and TPE discharged into the River Rhine indicates that NDM-5-producers may be widespread in the community and in the aquatic environment. Furthermore, OXA-48-producing *E. coli* D:ST38 was isolated from MWW. Its detection in MWW as well as HWW, TPI and TPE provides further evidence for the spread of this clone in the

community and healthy carriers, as described recently [25]. HWW contained a higher number of CPE isolates compared with MWW, including KPC- and OXA-48-producing *K. pneumoniae* belonging to CC258, a lineage that is the most prevalent cause of MDR *K. pneumoniae* infections in many countries [26,27]. HWW also contained a large number of OXA-48-producing *Citrobacter* spp. The occurrence of OXA-48-producing *Citrobacter* spp. in HWW over a period of several months may be due to their regular discharge from the hospital or to the persistence of these isolates in the wastewater environment. Of note are two *Citrobacter* spp. isolates (one from HWW and one from TPE) with an interesting genotypic and phenotypic similarity to a *C. freundii* urinary clinical isolate of a patient hospitalised previously in the University Hospital of Basel [28]. These isolates co-harboured *bla*_{OXA-48}, *bla*_{NDM-1}, *bla*_{SHV-12}, *bla*_{CTX-M-15} and *armA* and were resistant to β -lactams, the carbapenem compound ertapenem, aminoglycosides, fluoroquinolones and folic acid pathway inhibitors. For further comparison and clarification of the species identification, whole-genome sequencing is currently in progress and will be reported on later. This study has several limitations. First, not all morphologically identical colonies that were recovered from the water samples on selective plates were analysed. Thus, some resistant strains may have been missed. Therefore, the actual occurrence of CPE and MPB in wastewater may be even higher than observed. Second, it was not possible to directly compare the wastewater isolates with clinical isolates from the hospital, as no monitoring data or isolates from clinical cases from this hospital were available. The current findings highlight the need for further studies dedicated to correlating the presence of wastewater-associated CPE with human clinical isolates. Testing municipal and hospital wastewater for CPE or other antimicrobial-resistant

bacteria may also represent an approach to recognise emerging trends in resistance and the burden of faecal carriage in the population.

In TPI and TPE, carbapenemase-producing and methylase-producing isolates of clonal types that were identical to those found in MWW or HWW (mainly OXA-48-producing *E. coli* ST38 and OXA-48-producing *Citrobacter* spp.) were detected. This finding indicates that these isolates possess the ability to persist within wastewater and to survive the wastewater treatment process. Furthermore, some of the clones detected in TPE in this study have been described previously in clinical case reports or hospital outbreaks, such as OXA-181-producing *E. coli* ST410 [29] and OXA-48-producing *K. pneumoniae* ST29 and ST395 [30,31]. Other clones identified in this study such as *E. coli* ST393 and ST354 have been reported previously as ESBL-producers [32] but not, to our knowledge, as carbapenemase-producers. As mentioned in Section 3.1, a considerable fraction of CPE and MPB from the wastewater analysed in this study were commensal *E. coli* belonging to CC10. Strains belonging to this clonal complex have been observed to contribute significantly to the spread of ESBLs [33,34]. Hence, the detection of carbapenemases and 16S rRNA methylases in CC10 isolates in wastewater is of concern and supports the hypothesis of horizontal gene transmission by plasmid-mediated mechanisms among Enterobacteriaceae [32]. In contrast, no *E. coli* B2:ST131 isolates were detected. There is growing concern that this international extraintestinal pathogenic clone may be currently involved in the global dissemination of KPC-2 and other carbapenemases [35]. Data from the current study indicate that to date, the wastewater and TPE analysed in this study do not represent a reservoir for KPC-2-producing *E. coli* ST131. Although several studies have

described KPC- and VIM-producers in HWW [36], the current data indicate that OXA-48-producing Enterobacteriaceae, in particular *E. coli* and *Citrobacter* spp., may represent the greater threat to public health and environmental integrity.

In conclusion, wastewater is a reservoir of viable CPE and methylase-producing clones harbouring clinically relevant carbapenemases. Moreover, the purification process employed in the WWTP does not sufficiently reduce the burden of such MDR isolates, which are subsequently released into the aquatic environment.

Additional wastewater treatment processes are urgently required in order to reduce MDR bacteria of anthropogenic origin in wastewater, in particular primary treatment of hospital effluents prior to discharge into the sewage network.

Acknowledgements: The authors wish to thank the staff of the municipal works services of the city of Basel (Switzerland) for their help with sample collection.

Funding: This work was partly supported by the Swiss Federal Office of Public Health, Division Communicable Diseases.

Competing interests: None declared.

Ethical approval: Not required.

References

- [1] Falagas ME, Lourida P, Poulidakos P, Rafailidis PI, Tansarli GS. Antibiotic treatment of infections due to carbapenem-resistant Enterobacteriaceae: systematic evaluation of the available evidence. *Antimicrob Agents Chemother* 2014;58:654–63.
- [2] Hidalgo L, Hopkins KL, Gutierrez B, Ovejero CM, Shukla S, Douthwaite S, et al. Association of the novel aminoglycoside resistance determinant RmtF with NDM carbapenemase in Enterobacteriaceae isolated in India and the UK. *J Antimicrob Chemother* 2013;68:1543–50.
- [3] Nordmann P, Naas T, Poirel L. Global spread of carbapenemase-producing Enterobacteriaceae. *Emerg Infect Dis* 2011;17:1791–8.
- [4] Cantón R, Akóva M, Carmeli Y, Giske CG, Glupczynski Y, Gniadkowski M, et al. Rapid evolution and spread of carbapenemases among Enterobacteriaceae in Europe. *Clin Microbiol Infect* 2012;18:413–31.
- [5] Nordmann P, Poirel L. The difficult-to-control spread of carbapenemase producers among Enterobacteriaceae worldwide. *Clin Microbiol Infect* 2014;20:821–30.
- [6] Amos GCA, Hawkey PM, Gaze WH, Wellington EM. Waste water effluent contributes to the dissemination of CTX-M-15 in the natural environment. *J Antimicrob Chemother* 2014;69:1785–91.
- [7] Kwak Y-K, Colque P, Byfors S, Giske CG, Möllby R, Kühn I. Surveillance of antimicrobial resistance among *Escherichia coli* in wastewater in Stockholm during 1 year: does it reflect the resistance trends in the society? *Int J Antimicrob Agents* 2015;45:25–32.

- [8] Zhang X, Lü X, Zong Z. Enterobacteriaceae producing the KPC-2 carbapenemase from hospital sewage. *Diagn Microbiol Infect Dis* 2012;73:204–6.
- [9] White L, Hopkins KL, Meunier D, Perry CL, Pike R, Wilkinson P, et al. Carbapenemase-producing Enterobacteriaceae in hospital wastewater: a reservoir that may be unrelated to clinical isolates. *J Hosp Infect* 2016;93:145–51.
- [10] Baquero F, Martínez J-L, Cantón R. Antibiotics and antibiotic resistance in water environments. *Curr Opin Biotechnol* 2008;19:260–5.
- [11] Mollet C, Drancourt M, Raoult D. *rpoB* sequence analysis as a novel basis for bacterial identification. *Mol Microbiol* 1997;26:1005–11.
- [12] Clermont O, Bonacorsi S, Bingen E. Rapid and simple determination of the *Escherichia coli* phylogenetic group. *Appl Environ Microbiol* 2000;66:4555–8.
- [13] Wirth T, Falush D, Lan R, Colles F, Mensa P, Wieler LH, et al. Sex and virulence in *Escherichia coli*: an evolutionary perspective. *Mol Microbiol* 2006;60:1136–51.
- [14] Diancourt L, Passet V, Verhoef J, Grimont PA, Brisse S. Multilocus sequence typing of *Klebsiella pneumoniae* nosocomial isolates. *J Clin Microbiol* 2005;43:4178–82.
- [15] Ellington MJ, Kistler J, Livermore DM, Woodford N. Multiplex PCR for rapid detection of genes encoding acquired metallo- β -lactamases. *J Antimicrob Chemother* 2007;59:321–2.

- [16] Poirel L, Walsh TR, Cuvillier V, Nordmann P. Multiplex PCR for detection of acquired carbapenemase genes. *Diagn Microbiol Infect Dis* 2011;70:119–23.
- [17] Pitout JD, Thomson KS, Hanson ND, Ehrhardt AF, Moland ES, Sanders CC. β -Lactamases responsible for resistance to expanded-spectrum cephalosporins in *Klebsiella pneumoniae*, *Escherichia coli*, and *Proteus mirabilis* isolates recovered in South Africa. *Antimicrob Agents Chemother* 1998;42:1350–4.
- [18] Zurfluh K, Nüesch-Inderbinen M, Morach M, Zihler Berner A, Hächler H, Stephan R. Extended-spectrum β -lactamase-producing-Enterobacteriaceae in vegetables imported from the Dominican Republic, India, Thailand and Vietnam. *Appl Environ Microbiol* 2015;81:3115–20.
- [19] Doi Y, Arakawa Y. 16S ribosomal RNA methylation: emerging resistance mechanism against aminoglycosides. *Clin Infect Dis* 2007;45:88–94.
- [20] Liu Y-Y, Wang Y, Walsh TR, Yi LX, Zhang R, Spencer J, et al. Emergence of plasmid-mediated colistin resistance mechanism MCR-1 in animals and human beings in China: a microbiological and molecular biological study. *Lancet Infect Dis* 2015;16:161–8.
- [21] Clinical and Laboratory Standards Institute (CLSI). *Performance standards for antimicrobial susceptibility testing; twenty-third informational supplement*. Document M100-S23. Wayne, PA: CLSI; 2013.
- [22] Picão RC, Cardoso JP, Campana EH, Nicoletti AG, Petrolini FV, Assis DM, et al. The route of antimicrobial resistance from the hospital effluent to

- the environment: focus on the occurrence of KPC-producing *Aeromonas* spp. and Enterobacteriaceae in sewage. *Diagn Microbiol Infect Dis* 2013;76:80–5.
- [23] Munck C, Albertsen M, Telke A, Ellabaan M, Nielsen PH, Sommer MOA. Limited dissemination of the wastewater treatment plant core resistome. *Nat Commun* 2015;6:8452.
- [24] Hornsey M, Phee L, Wareham DW. A novel variant, NDM-5, of the New Delhi metallo- β -lactamase in a multidrug-resistant *Escherichia coli* ST648 isolate recovered from a patient in the United Kingdom. *Antimicrob Agents Chemother* 2011;55:5952–4.
- [25] Zurfluh K, Nüesch-Inderbinen MT, Poirel L, Nordmann P, Hächler H, Stephan R. Emergence of *Escherichia coli* producing OXA-48 β -lactamase in the community in Switzerland. *Antimicrob Resist Infect Control* 2015;4:9.
- [26] Munoz-Price LS, Poirel L, Bonomo RA, Schwaber MJ, Daikos GL, Cormican M et al. Clinical epidemiology of the global expansion of *Klebsiella pneumoniae* carbapenemases. *Lancet Infect Dis* 2013;13:785–96.
- [27] DeLeo FR, Chen L, Porcella SF, Martens CA, Kobayashi SD, Porter AR, et al. Molecular dissection of the evolution of carbapenem-resistant multilocus sequence type 258 *Klebsiella pneumoniae*. *Proc Natl Acad Sci U S A* 2014;111:4988–93.
- [28] Seiffert N, Perreten V, Hinic V, Frei R, Endimiani A, Carattoli A. *Citrobacter freundii* possessing *bla*_{OXA-48}, *bla*_{SHV-12}, *bla*_{CTX-M-15}, *bla*_{TEM-1}, and *armA* also carries the *bla*_{NDM-1} gene in a novel IncHI2 plasmid background. In: 25th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID); 25–28 April 2015; Copenhagen, Denmark. Basel, Switzerland:

European Society of Clinical Microbiology and Infectious Diseases; 2015
[abstract EV0088].

- [29] Liu Y, Feng Y, Wu W, Xie Y, Wang X, Zhang X, et al. First report of OXA-181-producing *Escherichia coli* in China and characterization of the isolate using whole-genome sequencing. *Antimicrob Agents Chemother* 2015;59:5022–5.
- [30] Cuzon G, Ouanich J, Gondret R, Naas T, Nordmann P. Outbreak of OXA-48-positive carbapenem-resistant *Klebsiella pneumoniae* isolates in France. *Antimicrob Agents Chemother* 2011;55:2420–3.
- [31] Zaman T, Aldrees M, Al Johani SM, Alrodayyan M, Aldughashem FA, Balkhy HH. Multi-drug carbapenem-resistant *Klebsiella pneumoniae* infection carrying the OXA-48 gene and showing variations in outer membrane protein 36 causing an outbreak in a tertiary care hospital in Riyadh, Saudi Arabia. *Int J Infect Dis* 2014;28:186–92.
- [32] Bajaj P, Singh NS, Viridi JS. *Escherichia coli* β -lactamases: what really matters. *Front Microbiol* 2016;7:417.
- [33] Izdebski R, Baraniak A, Fiett J, Adler A, Kazma M, Salomon J, et al. Clonal structure, extended-spectrum β -lactamases, and acquired AmpC-type cephalosporinases of *Escherichia coli* populations colonizing patients in rehabilitation centers in four countries. *Antimicrob Agents Chemother* 2013;57:309–16.
- [34] Oteo J, Diestra K, Juan C, Bautista V, Novais A, Pérez-Vázquez M, et al. Extended-spectrum β -lactamase-producing *Escherichia coli* in Spain belong to a large variety of multilocus sequence typing types, including ST10

complex/A, ST23 complex/A and ST131/B2. *Int J Antimicrob Agents* 2009;34:173–6.

- [35] Peirano G, Bradford PA, Kazmierczak KM, Badal RE, Hackel M, Hoban DJ, et al. Global incidence of carbapenemase-producing *Escherichia coli* ST131. *Emerg Infect Dis* 2014;20:1928–31.
- [36] Woodford N, Wareham DW, Guerra B, Teale C. Carbapenemase-producing Enterobacteriaceae and non-Enterobacteriaceae from animals and the environment: an emerging public health risk of our own making? *J Antimicrob Chemother* 2014;69:287–91.